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TECH CENTER



1600

RAW SEQUENCE LISTING

DATE: 06/23/2003

PATENT APPLICATION: US/09/647,140B

TIME: 14:00:58

Input Set : A:\Kruh 140 SequenceListing v2.txt

Output Set: N:\CRF4\06232003\I647140B.raw

3 <110> APPLICANT: Fox Chase Cancer Center
 4 Kruh, Gary D.
 5 Lee, Kun
 6 Belinsky, Martin G.
 7 Bain, Lisa J.
 9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
 10 Nucleic Acids and Methods of Use Thereof
 12 <130> FILE REFERENCE: FCCC 98-02
 14 <140> CURRENT APPLICATION NUMBER: 09/647,140B
 15 <141> CURRENT FILING DATE: 2001-05-21
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644
 18 <151> PRIOR FILING DATE: 1999-03-26
 20 <150> PRIOR APPLICATION NUMBER: 60/079,759
 21 <151> PRIOR FILING DATE: 1998-03-27
 23 <150> PRIOR APPLICATION NUMBER: 60/095,153
 24 <151> PRIOR FILING DATE: 1998-08-03
 26 <160> NUMBER OF SEQ ID NOS: 33
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 4231
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1

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38	ggccaccgcc	gcctgatcag	cgcgaccccg	gcccgcgccc	gccccgccc	gcaagatgct	120
39	gcccgtgtac	caggaggtga	agcccaaccc	gctgcaggac	gcgaacatct	gctcacgcgt	180
40	gttcttcttg	tggctcaatc	ccttgtttaa	aattggccat	aaacggagat	tagaggaaga	240
41	tgatatgtat	tcagtgtctg	cagaagaccg	ctcacagcac	cttgagagag	agttgcaagg	300
42	gttctgggat	aaagaagttt	taagagctga	gaatgacgca	cagaagcctt	ctttaacaag	360
43	agcaatcata	aagtgttact	ggaaatctta	tttagttttg	ggaattttta	cgtaattga	420
44	ggaaagtgcc	aaagtaatcc	agcccatatt	tttgggaaaa	attattaatt	attttgaaaa	480
45	ttatgatccc	atggattctg	tggctttgaa	cacagcgtac	gcctatgcc	cggtgctgac	540
46	tttttgcacg	ctcatttttg	ctatactgca	tcacttatat	ttttatcacg	ttcagtgtgc	600
47	tgggatgagg	ttacgagtag	ccatgtgcc	tatgatttat	cgaaggcac	ttcgtcttag	660
48	taacatggcc	atggggaaga	caaccacagg	ccagatagtc	aatctgctgt	ccaatgatgt	720
49	gaacaagttt	gacaggtga	cagtgttctt	acacttcctg	tgggcaggac	cactgcaggc	780
50	gatcgcatg	actgccctac	tctggatgga	gataggaata	tcgtgccttg	ctgggatggc	840
51	agttctaata	atttctctgc	ccttgcaaa	ctgttttggg	aagttgttct	catcactgag	900
52	gagtaaaact	gcaactttca	cgatgccag	gatcaggacc	atgaatgaag	ttataactgg	960
53	tataaggata	ataaaaatgt	acgcctggga	aaagtcattt	tcaaacttta	ttaccaattt	1020
54	gagaaagaag	gagattttcca	agattctgag	aagttcctgc	ctcaggggga	tgaatttggc	1080
55	ttcgtttttc	agtgaagca	aaatcatcgt	gtttgtgacc	ttcaccacct	acgtgtctct	1140
56	cggcagtggt	atcacagcca	gccgcgtgtt	cgtggcagtg	acgtgtatg	gggctgtgcg	1200

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57	gctgacgggtt	accctcttct	tcccctcagc	cattgagagg	gtgtcagagg	caatcgtcag	1260
58	catccgaaga	atccagacct	ttttgctact	tgatgagata	tcacagcgca	accgtcagct	1320
59	gccgtcagat	ggtaaaaaga	tggtgcatgt	gcaggatttt	actgcttttt	gggataaggc	1380
60	atcagagacc	ccaactctac	aaggcctttc	ctttactgtc	agacctggcg	aattgttagc	1440
61	tgtggtcggc	cccgtgggag	cagggaagtc	atcactgtta	agtgccgtgc	tcggggaatt	1500
62	ggccccaagt	cacgggctgg	tcagcgtgca	tggaagaatt	gcctatgtgt	ctcagcagcc	1560
63	ctgggtgttc	tcgggaactc	tgaggagtaa	tatttttatt	gggaagaaat	atgaaaagga	1620
64	acgatatgaa	aaagtcataa	aggcttgtgc	tctgaaaaag	gatttacagc	tgttggagga	1680
65	tggtgatctg	actgtgatag	gagatcgggg	aaccacgctg	agtggagggc	agaaagcacg	1740
66	ggtaaacctt	gcaagagcag	tgatatcaaga	tgctgacatc	tatctcctgg	acgatcctct	1800
67	cagtgcagta	gatgcggaag	ttagcagaca	cttggtcgaa	ctgtgtattt	gtcaaatttt	1860
68	gcatgagaag	atcacaattt	tagtgactca	tcagttgcag	tacctcaaag	ctgcaagtca	1920
69	gattctgata	ttgaaagatg	gtaaaatggt	gcagaagggg	acttacactg	agttcctaaa	1980
70	atctggtata	gatttttggt	cccttttaaa	gaaggataat	gaggaaagtg	aacaacctcc	2040
71	agttccagga	actcccacac	taaggaatcg	taccttctca	gagtcttcgg	tttgggtctca	2100
72	acaatcttct	agaccctcct	tgaaagatgg	tgctctggag	agccaagata	cagagaatgt	2160
73	cccagttaca	ctatcagagg	agaaccgttc	tgaaggaaaa	gttggttttc	aggcctataa	2220
74	gaattacttc	agagctggtg	ctcactggat	tgtcttcatt	ttccttattc	tcctaaacac	2280
75	tgcagctcag	gttgcctatg	tgcttcaaga	ttggtggcct	tcatactggg	caaacaaaca	2340
76	aagtatgcta	aatgtcactg	taaatggagg	aggaaatgta	accgagaagc	tagatcttaa	2400
77	ctggtactta	ggaattttatt	caggtttaac	tgtagctacc	gttctttttg	gcatagcaag	2460
78	atctctattg	gtattctacg	tccttggtta	ctcttcacaa	actttgcaca	acaaaatgtt	2520
79	tgagtcaatt	ctgaaagctc	cggattattt	ctttgataga	aatccaatag	gaagaatttt	2580
80	aaatcgtttc	tccaaagaca	ttggacactt	ggatgatttg	ctgccgctga	cgtttttaga	2640
81	tttcatccag	acattgtctac	aagtggttgg	tgtggtctct	gtggctgtgg	ccgtgattcc	2700
82	ttggatcgca	atacccttgg	ttccccttgg	aatcattttc	atttttcttc	ggcgatattt	2760
83	tttggaacg	tcaagagatg	tgaagcgcct	ggaatctaca	actcggagtc	cagtgttttc	2820
84	ccacttgtca	tcttctctcc	aggggctctg	gaccatccgg	gcatacaaag	cagaagagag	2880
85	gtgtcaggaa	ctgtttgatg	cacaccagga	tttacattca	gaggcttggt	tcttgttttt	2940
86	gacaacgtcc	cgctggttcg	ccgtccgtct	ggatgccatc	tgtgccatgt	ttgtcatcat	3000
87	cgttgccctt	gggtccctga	ttctggcaaa	aactctggat	gccgggcagg	ttggtttggc	3060
88	actgtcctat	gccctcacgc	tcatggggat	gtttcagtg	tgtgttcgac	aaagtgtctg	3120
89	agttgagaat	atgatgatct	cagtagaaag	ggtcattgaa	tacacagacc	ttgaaaaaga	3180
90	agcaccttgg	gaatatcaga	aacgccacc	accagcctgg	ccccatgaag	gagtataat	3240
91	ctttgacaat	gtgaacttca	tgtacagtcc	aggtgggcct	ctggtactga	agcatctgac	3300
92	agcactcatt	aaatcacaag	aaaaggttgg	cattgtggga	agaaccggag	ctggaaaaag	3360
93	ttccctcatc	tcagcccttt	ttagattgtc	agaaccgaa	ggtaaaattt	ggattgataa	3420
94	gatcttgaca	actgaaattg	gacttcacga	tttaagggaag	aaaatgtcaa	tcatactca	3480
95	ggaacctgtt	ttgttctact	gaacaatgag	gaaaaacctg	gatcccttta	aggagcacac	3540
96	ggatgaggaa	ctgtggaatg	ccttacaaga	ggtacaactt	aaagaaacca	ttgaagatct	3600
97	tcctggtaaa	atggatactg	aattagcaga	atcaggatcc	aatttttagtg	ttggacaaag	3660
98	acaactggtg	tgccttgcca	gggcaattct	caggaaaaat	cagatattga	ttattgatga	3720
99	agcgacggca	aatgtggatc	caagaactga	tgagttaata	caaaaaaaaa	tccgggagaa	3780
100	atttgcccac	tgcaccgtgc	taaccattgc	acacagattg	aacaccatta	ttgacagcga	3840
101	caagataatg	gttttagatt	caggaagact	gaaagaatat	gatgagccgt	atgttttgct	3900
102	gcaaaataaa	gagagcctat	tttacaagat	ggtgcaacaa	ctgggcaagg	cagaagccgc	3960
103	tgccctcact	gaaacagcaa	aacaggatata	cttcaaaaga	aattatccac	atattgggtca	4020
104	cactgaccac	atggttacaa	acacttccaa	tggacagccc	tcgaccttaa	ctattttcga	4080
105	gacagcactg	tgaatccaac	caaaatgtca	agtcctgttc	gaaggcattt	tccactagtt	4140

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106 tttggactat gtaaaccaca ttgtactttt ttttactttg gcaacaaata tttatacata 4200
107 caagatgcta gttcatttga atatttctcc c 4231
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 1325
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
116 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
117 1 5 10 15
118 Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
119 20 25 30
120 Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
121 35 40 45
122 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
123 50 55 60
124 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
125 65 70 75 80
126 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
127 85 90 95
128 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
129 100 105 110
131 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
132 115 120 125
133 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
134 130 135 140
135 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
136 145 150 155 160
137 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
138 165 170 175
139 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
140 180 185 190
141 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
142 195 200 205
143 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
144 210 215 220
145 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
146 225 230 235 240
147 Met Ala Val Leu Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
148 245 250 255
149 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
150 260 265 270
151 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
152 275 280 285
153 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
154 290 295 300
155 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
156 305 310 315 320
157 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
158 325 330 335

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```

159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
160          340          345          350
161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
162          355          360          365
163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
164          370          375          380
165 Arg Ile Gln Thr Phe Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
166          385          390          395          400
167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
168          405          410          415
169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
170          420          425          430
171 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
172          435          440          445
173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
174          450          455          460
175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
176          465          470          475          480
177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
178          485          490          495
179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
180          500          505          510
181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
182          515          520          525
183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
184          530          535          540
185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
186          545          550          555          560
187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
188          565          570          575
189 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
190          580          585          590
191 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
192          595          600          605
193 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
194          610          615          620
196 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
197          625          630          635          640
198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
199          645          650          655
200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
201          660          665          670
202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
203          675          680          685
204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
205          690          695          700
206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
207          705          710          715          720
208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser

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209				725					730				735		
210	Tyr	Trp	Ala	Asn	Lys	Gln	Ser	Met	Leu	Asn	Val	Thr	Val	Asn	Gly Gly
211				740					745				750		
212	Gly	Asn	Val	Thr	Glu	Lys	Leu	Asp	Leu	Asn	Trp	Tyr	Leu	Gly	Ile Tyr
213				755				760					765		
214	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly	Ile	Ala	Arg	Ser Leu
215				770				775					780		
216	Leu	Val	Phe	Tyr	Val	Leu	Val	Asn	Ser	Ser	Gln	Thr	Leu	His	Asn Lys
217						790					795				800
218	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu	Phe	Phe	Asp	Arg Asn
219					805						810				815
220	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	Asp	Ile	Gly	His Leu
221				820					825					830	
222	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe	Ile	Gln	Thr	Leu Leu
223				835				840					845		
224	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala	Val	Ile	Pro	Trp Ile
225				850				855					860		
226	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe	Ile	Phe	Leu	Arg Arg
227						870					875				880
228	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg	Leu	Glu	Ser	Thr Thr
229					885					890					895
230	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser	Leu	Gln	Gly	Leu Trp
231				900					905						910
232	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys	Gln	Glu	Leu	Phe Asp
233				915				920					925		
234	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe	Leu	Phe	Leu	Thr Thr
235				930			935					940			
236	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile	Cys	Ala	Met	Phe Val
237						950					955				960
238	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala	Lys	Thr	Leu	Asp Ala
239					965					970					975
240	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu	Thr	Leu	Met	Gly Met
241				980					985					990	
242	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val	Glu	Asn	Met	Met Ile
243				995				1000					1005		
244	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu	Glu	Lys	Glu	Ala Pro
245				1010				1015					1020		
246	Trp	Glu	Tyr	Gln	Lys	Arg	Pro	Pro	Pro	Ala	Trp	Pro	His	Glu	Gly Val
247						1030					1035				1040
248	Ile	Ile	Phe	Asp	Asn	Val	Asn	Phe	Met	Tyr	Ser	Pro	Gly	Gly	Pro Leu
249					1045					1050					1055
250	Val	Leu	Lys	His	Leu	Thr	Ala	Leu	Ile	Lys	Ser	Gln	Glu	Lys	Val Gly
251				1060					1065					1070	
252	Ile	Val	Gly	Arg	Thr	Gly	Ala	Gly	Lys	Ser	Ser	Leu	Ile	Ser	Ala Leu
253				1075				1080					1085		
254	Phe	Arg	Leu	Ser	Glu	Pro	Glu	Gly	Lys	Ile	Trp	Ile	Asp	Lys	Ile Leu
255				1090				1095					1100		
256	Thr	Thr	Glu	Ile	Gly	Leu	His	Asp	Leu	Arg	Lys	Lys	Met	Ser	Ile Ile
257						1110					1115				1120

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 18
Seq#:16; N Pos. 4,7,10,13,16,19
Seq#:17; N Pos. 23,29
Seq#:18; N Pos. 9,18